Human papillomavirus (HPV) is the main cause of cervical cancer, which is one of the most common cancers in women worldwide. Current HPV analysis methods are limited to either analysis of HPV variation or chromosomal integration. TaME-seq (tagmentation-assisted multiplex PCR enrichment sequencing) is an innovative and cost-effective sequencing approach, which combines tagmentation and multiplex PCR enrichment for simultaneous analysis of HPV variation and chromosomal integration, and it can also be adapted to other viruses. Thus, it provides higher clinical specificity than any other HPV test on the market.

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**Key benefits**

- Higher clinical specificity than any other test on the market
- Can be used to determine if the patient has a transient or persistent HPV infection where the latter is associated with a higher cancer risk
- Innovative library preparation strategy and an in-house bioinformatics pipeline named TaME-seq
- Simultaneous HPV genomic variability and integration analysis
- Applicable to large sample cohorts leading to reduced sequencing costs

**Key Publication**


**Patents**

Patent pending for TaME-sequencing